

[SEQUENCE LISTING]

INFORMATION FOR SEQ ID NO:1

Length of sequence: 120

5 Type of sequence: amino acid

Topology: linear

Kind of sequence: peptide

Sequence description:

Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
 10 1 5 10 15
 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp
 20 25 30
 Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly
 35 40 45
 15 Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys
 50 55 60
 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
 20 85 90 95
 Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

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INFORMATION FOR SEQ ID NO:2

Length of sequence: 360

Type of sequence: nucleic acid

Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

5 Origin:

Mouse

Feature of sequence:

Identification method: E

Sequence description:

10	GTG CAG CTG CAG GAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCC TCA	48
	GTG AAG ATT TCC TGC AAG GCT TCT GGC TAT GCA TTC AGT AGC TCC TGG	96
	ATG AAC TGG GTG AAG CAG AGG CCT GGA AAG GGT CTT GAG TGG ATT GGA	144
	CGA ATT TAT CCT GGA GAT GGA GAT ACT AAC GAC AAC GGG AAG TTC AAG	192
	GGC AAG GCC ACA CTG ACC GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG	240
15	CAA CTC AGC AGT CTG ACA TCT GAG GAC TCT GCG GTC TAC TTC TGT GCA	288
	AGA TCG TAT TAC TAC GAT GGT AGC CCC TGG TTT ACT TAC TGG GGC CAA	336
	GGG ACC ACG GTC ACC GTC TCC TCA	360

INFORMATION FOR SEQ ID NO:3

20 Length of sequence: 108

Type of sequence: amino acid

Topology: linear

Kind of sequence: peptide

Sequence description:

25 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr

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Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 5 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 10 100 105

INFORMATION FOR SEQ ID NO:4

Length of sequence: 324

Type of sequence: nucleic acid

15 Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

Mouse

20 Feature of sequence:

Identification method: E

Sequence description:

GAC ATC CAG ATG ACG CAG TCT CCA TCC TCC CTG TCT GCC TCT CTG GGA 48
 GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAT ATT AGC AAT TAT 96
 25 TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT AAA CTC CTG ATC 144
 TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA AGG TTC AGT GGC 192
 AGT GGG TCT GGG ACA GAT TAT TCT CTC ACC ATC AGC AAC CTG GAA CCT 240

GAA GAT ATT GCC ACT TAC TTT TGT CAG CAA TAT AGT GAA TTT CCG TGG 288
 ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG 324

INFORMATION FOR SEQ ID NO:5

5 Length of sequence: 118

Type of sequence: amino acid

Topology: linear

Kind of sequence: peptide

Sequence description:

10 Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser
 1 5 10 15
 Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr Trp
 20 25 30
 Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
 15 35 40 45
 Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
 50 55 60
 Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 20 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
 85 90 95
 Arg Tyr Arg Asp Tyr Asp Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 25 115

INFORMATION FOR SEQ ID NO:6

Length of sequence: 354

Type of sequence: nucleic acid

Strandedness: double

5 Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

Mouse

Feature of sequence:

10 Identification method: E

Sequence description:

	GTG CAG CTG CAG CAG TCA GGA GCT GAG CTG GTA AGG CCT GGG ACT TCA	48
	GTG AAG ATG TCC TGC AAG GCT GCT GGA TAC ACC TTC ACT AAC TAC TGG	96
	ATA GGT TGG GTA AAG CAG AGG CCT GGA CAT GGC CTT GAG TGG ATT GGA	144
15	TAT CTT TAC CCT GGA GGT CTT TAT ACT AAC TAC AAT GAG AAG TTC AAG	192
	GGC AAG GCC ACA CTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC ATG	240
	CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCC ATC TAT TAC TGT GCA	288
	AGA TAC AGG GAT TAC GAC TAT GCT ATG GAC TAC TGG GGC CAA GGG ACC	336
	ACG GTC ACC GTC TCC TCA	354

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INFORMATION FOR SEQ ID NO:7

Length of sequence: 113

Type of sequence: amino acid

Topology: linear

25 Kind of sequence: peptide

Sequence description:

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly
 1 5 10 15
 Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser
 20 25 30
 5 Asp Gly Phe Thr Tyr Leu Gly Trp Cys Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 10 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser
 85 90 95
 Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 15 Arg

INFORMATION FOR SEQ ID NO:8

Length of sequence: 339

20 Type of sequence: nucleic acid

Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

25 Mouse

Feature of sequence:

Identification method: E

Sequence description:

GAT GTT TTG ATG ACC CAA ACT CCA CTC TCT CTG CCT GTC AAT ATT GGA 48
 GAT CAA GCC TCT ATC TCT TGC AAG TCT ACT AAG AGC CTT CTG AAT AGT 96
 GAT GGA TTC ACT TAT TTG GGC TGG TGC CTG CAG AAG CCA GGC CAG TCT 144
 5 CCA CAG CTC CTA ATA TAT TTG GTT TCT AAT CGA TTT TCT GGA GTT CCA 192
 GAC AGG TTC AGT GGT AGT GGG TCA GGG ACA GAT TTC ACC CTC AAG ATC 240
 AGC AGA GTG GAG GCT GAG GAT TTG GGA GTT TAT TAT TGC TTC CAG AGT 288
 AAC TAT CTT CCT CTT ACG TTC GGA TCG GGG ACC AAG CTG GAA ATA AAA 336
 CGG 339

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INFORMATION FOR SEQ ID NO:9

Length of sequence: 116

Type of sequence: amino acid

Topology: linear

15 Kind of sequence: peptide

Sequence description:

Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
 1 5 10 15
 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp
 20 20 25 30
 Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly
 35 40 45
 Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
 50 55 60
 25 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
 85 90 95

Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val

100

105

110

Thr Val Ser Ser

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INFORMATION FOR SEQ ID NO:10

Length of sequence: 348

Type of sequence: nucleic acid

Strandedness: double

10 Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

Mouse

Feature of sequence:

15 Identification method: E

Sequence description:

GTG AAG CTG CAG GAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCC TCA 48

GTG AAG ATT TCC TGC AAG GCT TCT GGC TAT GCA TTC AGT AGC TCC TGG 96

ATG AAC TGG GTG AAA CAG AGG CCT GGG AAG GGT CTT GAG TGG ATT GGA 144

20 CGG ATT TAT CCT GTA AAT GGA GAT ACT AAC TAC AAT GGG AAG TTC AAG 192

GGC AAG GCC ACA CTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG 240

CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAC TTC TGT GCA 288

ACC GAT GGT TAC TGG TAC TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC 336

ACC GTC TCC TCA 348

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INFORMATION FOR SEQ ID NO:11

Length of sequence: 118

Type of sequence: amino acid

Topology: linear

Kind of sequence: peptide

Sequence description:

5 Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser
 1 5 10 15
 Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr
 20 25 30
 Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met
 10 35 40 45
 Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu
 65 70 75 80
 15 Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95
 Val Tyr Tyr Tyr Asp Gly Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 20 115

INFORMATION FOR SEQ ID NO:12

Length of sequence: 354

Type of sequence: nucleic acid

25 Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
 65 70 75 80
 Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
 85 90 95
 5 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

INFORMATION FOR SEQ ID NO:14

Length of sequence: 336

10 Type of sequence: nucleic acid

Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

15 Mouse

Feature of sequence:

Identification method: E

Sequence description:

	GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT GTG TCT CTA AGG	48
20	CAG AGG GCC ACC ATA TCC TGC AGA GCC AGT GAA GGT GTT GAT AGT TAT	96
	GGC ATT AGT TTT ATG CAC TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC	144
	AAA CTC CTC ATC TAT CGT GCA TCC TAC CTA AAA TCT GGG GTC CCT GCC	192
	AGG TTC AGT GGT AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC ATT GAT	240
	CCT GTG GAG GCT GAT GAT GCT GCA ACC TAT TAC TGT CAG CAA AAT AAT	288
25	GAG GAT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG	336

INFORMATION FOR SEQ ID NO:15

Length of sequence: 117

Type of sequence: amino acid

Topology: linear

5 Kind of sequence: peptide

Sequence description:

Val Gln Leu Gln Glu Ser Gly Ala Glu Pro Ala Lys Pro Gly Ala Ser
 1 5 10 15
 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Trp
 10 20 25 30
 Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45
 Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys
 50 55 60
 15 Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Gln Leu Ile Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Arg Gly Asn Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 20 100 105 110
 Val Thr Val Ser Ser
 115

INFORMATION FOR SEQ ID NO:16

25 Length of sequence: 351

Type of sequence: nucleic acid

Strandedness: double

Origin:

Mouse

5 Feature of sequence:

Identification method: E

Sequence description:

	GTG CAG CTG CAG GAG TCT GGG GCT GAA CCG GCA AAA CCT GGG GCC TCA	48
	GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT ACC TAC TGG	96
10	ATG CAC TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG ATT GGA	144
	TAC ATT AAT CCT AGC AGT GGT TAT ACT GAG TAC AAT CAG AAG TTC AAG	192
	GAC AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG	240
	CAA CTA ATC AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT TAC TGT GCA	288
	AGA AGG GGT AAT TAC TAC TAC TTT GAC TAC TGG GGC CAA GGG ACC ACG	336
15	GTC ACC GTC TCC TCA	351

INFORMATION FOR SEQ ID NO:17

Length of sequence: 105

Type of sequence: amino acid

20 **Topology: linear**

Kind of sequence: peptide

Sequence description:

Asp Val Leu Met Thr Gln Thr Pro Lys Phe Leu Pro Val Ser Ala Gly
 1 5 10 15
 25 Asp Arg Val Thr Met Thr Cys Lys Ala Ser Gln Ser Val Gly Asn Asn
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Val
 65 70 75 80
 5 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ser Ser Pro Tyr
 85 90 95
 Thr Phe Gly Ser Gly Thr Lys Leu Glu
 100 105

10 INFORMATION FOR SEQ ID NO:18

Length of sequence: 315

Type of sequence: nucleic acid

Strandedness: double

Topology: linear

15 Kind of sequence: cDNA to mRNA

Origin:

Mouse

Feature of sequence:

Identification method: E

20 Sequence description:

GAT GTT TTG ATG ACC CAA ACT CCA AAA TTC CTG CCT GTA TCA GCA GGA 48
 GAC AGG GTT ACC ATG ACC TGC AAG GCC AGT CAG AGT GTG GGT AAT AAT 96
 GTG GCC TGG TAC CAA CAG AAG CCA GGA CAG TCT CCT AAA CTG CTG ATA 144
 TAC TAT ACA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
 25 AGT GGA TCT GGG ACA GAT TTC ACT TTC ACC ATC AGC AGT GTG CAG GTT 240
 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG CAT TAT AGC TCT CCG TAT 288
 ACG TTC GGA TCG GGG ACC AAG CTG GAG 315

INFORMATION FOR SEQ ID NO:19

Length of sequence: 121

Type of sequence: amino acid

Topology: linear

5 Kind of sequence: peptide

Sequence description:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
 10 20 25 30
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe
 50 55 60
 15 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly
 20 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ala
 115 120

INFORMATION FOR SEQ ID NO:20

25 Length of sequence: 363

Type of sequence: nucleic acid

Strandedness: double

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
 65 70 75 80
 5 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

10 INFORMATION FOR SEQ ID NO:22

Length of sequence: 324

Type of sequence: nucleic acid

Strandedness: double

Topology: linear

15 Kind of sequence: cDNA to mRNA

Origin:

Mouse

Feature of sequence:

Identification method: E

20 Sequence description:

GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT GCC TCT CTG GGA 48
 GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAT ATT AGC AAT TAT 96
 TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT AAA CTC CTG ATC 144
 TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA AGG TTC AGT GGC 192
 25 AGT GGG TCT GGG ACA GAT TAT TCT CTC ACC ATC AGC AAC CTG GAA CCT 240
 GAA GAT ATT GCC ACT TAC TTT TGT CAG CAA TAT AGT GAA TTT CCG TGG 288
 ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG 324

INFORMATION FOR SEQ ID NO:23

Length of sequence: 119

Type of sequence: amino acid

Topology: linear

5 Kind of sequence: peptide

Sequence description:

Gln Val His Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr
 10 20 25 30
 Trp Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 15 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Arg Asp Tyr Asp Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 20 100 105 110
 Thr Ser Val Thr Val Ser Ser
 115

INFORMATION FOR SEQ ID NO:24

25 Length of sequence: 357

Type of sequence: nucleic acid

Strandedness: double

Origin:

Mouse

Identification method: E

CAG GTC CAC CTG CAG CAG TCT GGA GCT GAG CTG GTA AGG CCT GGG ACT	48
TCA GTG AAG ATG TCC TGC AAG GCT GCT GGA TAC ACC TTC ACT AAC TAC	96
TGG ATA GGT TGG GTA AAG CAG AGG CCT GGA CAT GGC CTT GAG TGG ATT	144
GGA TAT CTT TAC CCT GGA GGT CTT TAT ACT AAC TAC AAT GAG AAG TTC	192
AAG GGC AAG GCC ACA CTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC	240
ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCC ATC TAT TAC TGT	288
GCA AGA TAC AGG GAT TAC GAC TAT GCT ATG GAC TAC TGG GGT CAA GGA	336
ACC TCA GTC ACC GTC TCC TCA	357

Type of sequence: amino acid

Sequence description:

1 5 10 15

20 25 30

35 40 45

Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 5 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser
 85 90 95
 Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 Arg

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INFORMATION FOR SEQ ID NO:26

Length of sequence: 339

Type of sequence: nucleic acid

15 Strandedness: double

Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

Mouse

20 Feature of sequence:

Identification method: E

Sequence description:

GAT GTT GTT CTG ACC CAA ACT CCA CTC TCT CTG CCT GTC AAT ATT GGA 48
 GAT CAA GCC TCT ATC TCT TGC AAG TCT ACT AAG AGC CTT CTG AAT AGT 96
 25 GAT GGA TTC ACT TAT TTG GGC TGG TGC CTG CAG AAG CCA GGC CAG TCT 144
 CCA CAG CTC CTA ATA TAT TTG GTT TCT AAT CGA TTT TCT GGA GTT CCA 192
 GAC AGG TTC AGT GGT AGT GGG TCA GGG ACA GAT TTC ACC CTC AAG ATC 240

AGC AGA GTG GAG GCT GAG GAT TTG GGA GTT TAT TAT TGC TTC CAG AGT 288
 AAC TAT CTT CCT CTT ACG TTC GGA TCG GGG ACC AAG CTG GAA ATA AAA 336
 CGG 339

5 INFORMATION FOR SEQ ID NO:27

Length of sequence: 117

Type of sequence: amino acid

Topology: linear

Kind of sequence: peptide

10 Sequence description:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
 20 25 30
 15 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 20 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
 100 105 110
 25 Val Thr Val Ser Ser
 115

INFORMATION FOR SEQ ID NO:28

Length of sequence: 351

Type of sequence: nucleic acid

Strandedness: double

5 Topology: linear

Kind of sequence: cDNA to mRNA

Origin:

Mouse

Feature of sequence:

10 Identification method: E

Sequence description:

	CAG GTT CAG CTG CAG CAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCC	48
	TCA GTG AAG ATT TCC TGC AAG GCT TCT GGC TAT GCA TTC AGT AGC TCC	96
	TGG ATG AAC TGG GTG AAA CAG AGG CCT GGG AAG GGT CTT GAG TGG ATT	144
15	GGA CGG ATT TAT CCT GTA AAT GGA GAT ACT AAC TAC AAT GGG AAG TTC	192
	AAG GGC AAG GCC ACA CTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC	240
	ATG CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAC TTC TGT	288
	GCA ACC GAT GGT TAC TGG TAC TTC GAT GTC TGG GGC GCA GGG ACC ACG	336
	GTC ACC GTC TCC TCA	351

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INFORMATION FOR SEQ ID NO:29

Length of sequence: 108

Type of sequence: amino acid

Topology: linear

25 Kind of sequence: peptide

Sequence description:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly

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Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ile Tyr
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 5 Tyr Gly Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ser Asp Tyr Tyr Cys Val Gln Ser Tyr Ser Tyr Pro Trp
 10 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

INFORMATION FOR SEQ ID NO:30

15 Length of sequence: 324
 Type of sequence: nucleic acid
 Strandedness: double
 Topology: linear
 Kind of sequence: cDNA to mRNA
 20 Origin:
 Mouse
 Feature of sequence:
 Identification method: E
 Sequence description:

25 AAC ATT GTA ATG ACC CAA TCT CCC AAA TCC ATG TCC ATG TCA GTA GGA 48
 GAG AGG GTC ACC TTG AGC TGC AAG GCC AGT GAG AAT GTG GAT ATT TAT 96
 GTA TCC TGG TAT CAA CAG AAA CCA GAG CAG TCT CCT AAA CTG CTG ATA 144

TAC GGG ACA TCC AAC CGG TAC ACT GGG GTC CCC GAT CGC TTC ACA GGC	192
AGT GGA TCT GCA ACA GAT TTC ACT CTG ACC ATC AGC AAT GTG CAG GCT	240
GAA GAC CTT TCA GAT TAT TAC TGT GTA CAG AGT TAC AGC TAT CCG TGG	288
ACA TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG	324

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INFORMATION FOR SEQ ID NO:31

Length of sequence: 14

Type of sequence: amino acid

Topology: linear

10 Kind of sequence: peptide

Sequence description:

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln

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